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RAW SEQUENCE LISTING

DATE: 12/05/2001

PATENT APPLICATION: US/09/851,138A ✓

TIME: 11:39:07

Input Set : N:\Crf3\RULE60\09851138A.txt

Output Set: N:\CRF3\12052001\I851138A.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: MAERTENS, GEERT

7 STUYVER, LIEVEN

9 (ii) TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
 10 AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
 11 AGENTS

13 (iii) NUMBER OF SEQUENCES: 207

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: ARNOLD, WHITE & DURKEE

17 (B) STREET: P.O. BOX 4433

18 (C) CITY: HOUSTON

19 (D) STATE: TEXAS

20 (E) COUNTRY: USA

21 (F) ZIP: 77210-4433

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: Microsoft Word 6.0 / ASCII text output

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/851,138A

C--> 31 (B) FILING DATE: 09-May-2001

C--> 41 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 08/836,075

35 (B) FILING DATE: 1998-01-02

38 (A) APPLICATION NUMBER: EP 94870166.9

39 (B) FILING DATE: 21 Oct 1994

42 (A) APPLICATION NUMBER: EP 95870076.7

43 (B) FILING DATE: 28 Jun 1995

C--> 45 (viii) ATTORNEY/AGENT INFORMATION:

46 (A) NAME: KAMMERER, PATRICIA A.

47 (B) REGISTRATION NUMBER: 29,775

48 (C) REFERENCE/DOCKET NUMBER: INNS:004

50 (2) INFORMATION FOR SEQ ID NO: 1:

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 327 base pairs

54 (B) TYPE: nucleic acid

55 (C) STRANDEDNESS: single

56 (D) TOPOLOGY: linear

58 (ii) MOLECULE TYPE: cDNA

60 (iii) HYPOTHETICAL: NO

C--> 62 (iv) ANTI-SENSE: NO

67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

69 ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CCGCCCTCAK 60

71 GSGGTNNNNN NNCCGGGTGG CGGTCAGATC GTTGGTGGAG TTTACCTGTT GCCGCGCAGG 120

73 GGCCCCAGGN NGGGTGTGCG CGCGACTAGG AAGACTTCCG AGCGGTCACA ACCTCGTGGC 180

ENTERED

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75 AGGCGACAGC CTATCCCCAA GGCTCGYCGG YCCGAGGGCA GGTCCCTGGGC TCAGCCCCGGG      240
77 TATCCTTGGC CCCTCTATGG CAATGAGGGC TGCGGGTGGG CGGGNTGGCT CCTGTCCCCC      300
79 CGCGGCTCTC GGCCCAATTG GGGCCCC      327
81 (2) INFORMATION FOR SEQ ID NO: 2:
83     (i) SEQUENCE CHARACTERISTICS:
84         (A) LENGTH: 109 amino acids
85         (B) TYPE: amino acid
86         (D) TOPOLOGY: linear
88     (ii) MOLECULE TYPE: peptide
92     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
94     Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
95     1          5          10          15
W--> 97     Arg Arg Pro Xaa Xaa Xaa Xaa Xaa Pro Gly Gly Gly Gln Ile Val Gly
98           20          25          30
W--> 100     Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Xaa Gly Val Arg Ala
101          35          40          45
103     Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
104          50          55          60
W--> 106     Ile Pro Lys Ala Xaa Arg Xaa Glu Gly Arg Ser Trp Ala Gln Pro Gly
107          65          70          75          80
W--> 109     Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Xaa Trp
110           85          90          95
112     Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro
113           100         105
115 (2) INFORMATION FOR SEQ ID NO: 3:
117     (i) SEQUENCE CHARACTERISTICS:
118         (A) LENGTH: 447 base pairs
119         (B) TYPE: nucleic acid
120         (C) STRANDEDNESS: single
121         (D) TOPOLOGY: linear
123     (ii) MOLECULE TYPE: cDNA
125     (iii) HYPOTHETICAL: NO
C--> 127     (iv) ANTI-SENSE: NO
131     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
133 GACGGCGTGA ACTATGCAAC AGGGAAGTTG CCCGGTTGCT CTTTCTCTAT CTTCTCTTGT      60
135 GCTTTGCTGT CCTGCTTGAC GGTTCGAACK ACCGCTCACG AGGTGCGCAA CGCATCCGGG      120
137 GTGTATCATG TCACCAACGA CTGTTCCAAC TCGAGCATCA TCTATGAGAT GGACGGTATG      180
139 ATCATGCACT ACCCAGGGTG CGTGCCCTGC GTTCGGGAGG ATAACCATCT CCGCTGCTGG      240
141 ATGGCGCTCA CCCCCACGCT TGCGGTCAAA AAYGCTAGTG TCCCCACTRC GGCAATCCGA      300
143 CGTCACGTCG ACTTGCTTGT TGGGGGNNCC ACGTTCTGTT CCGCTATGTA CGTGGGRGAC      360
145 CTTTGCGGGT CTGTCTTCCT CGCTGGCCAG CTATTCACCT TTTCACCCCG CATGCACCAT      420
147 ACAACGCAGG AGTGCAACTG CTCAATC      447
149 (2) INFORMATION FOR SEQ ID NO: 4:
151     (i) SEQUENCE CHARACTERISTICS:
152         (A) LENGTH: 149 amino acids
153         (B) TYPE: amino acid
154         (D) TOPOLOGY: linear
156     (ii) MOLECULE TYPE: peptide
160     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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```

162   Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
163   1           5           10           15
W--> 165   Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Xaa Thr Ala
166           20           25           30
168   His Glu Val Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp Cys
169           35           40           45
171   Ser Asn Ser Ser Ile Ile Tyr Glu Met Asp Gly Met Ile Met His Tyr
172           50           55           60
174   Pro Gly Cys Val Pro Cys Val Arg Glu Asp Asn His Leu Arg Cys Trp
175           65           70           75           80
W--> 177   Met Ala Leu Thr Pro Thr Leu Ala Val Lys Xaa Ala Ser Val Pro Thr
178           85           90           95
W--> 180   Xaa Ala Ile Arg Arg His Val Asp Leu Leu Val Gly Xaa Xaa Thr Phe
181           100          105          110
W--> 183   Cys Ser Ala Met Tyr Val Xaa Asp Leu Cys Gly Ser Val Phe Leu Ala
184           115          120          125
186   Gly Gln Leu Phe Thr Phe Ser Pro Arg Met His His Thr Thr Gln Glu
187           130          135          140
189   Cys Asn Cys Ser Ile
190           145
192 (2) INFORMATION FOR SEQ ID NO: 5:
194   (i) SEQUENCE CHARACTERISTICS:
195       (A) LENGTH: 327 base pairs
196       (B) TYPE: nucleic acid
197       (C) STRANDEDNESS: single
198       (D) TOPOLOGY: linear
200   (ii) MOLECULE TYPE: cDNA
202   (iii) HYPOTHETICAL: NO
C--> 204   (iv) ANTI-SENSE: NO
208   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
210 ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CCGCCCACAG      60
212 GACGTCAAGN TCCCGGGTGG TGGTCAGATC GTTGGTGGAG TTTACCTGTT GCCGCGCAGG      120
214 GGCCCCAGGT TGGGTGTGCG CGCGACCAGG AAGACTTCCG AGCGGTCGCA GCCTCGTGAC      180
216 AGGCGACAGC CTATTCCTAA GGCTCGCCAG TCCGATGGCA GNNCCTGGGC TCAGCCAGGG      240
218 CATCCCTGGC CCCTCTATGG CAATGAGGGC TCGGATGGG CGGGATGGCT CCTGTCCCCC      300
220 CGCGGCTCTC GGCCCAGTTG GGGCCCC      327
222 (2) INFORMATION FOR SEQ ID NO: 6:
224   (i) SEQUENCE CHARACTERISTICS:
225       (A) LENGTH: 109 amino acids
226       (B) TYPE: amino acid
227       (D) TOPOLOGY: linear
229   (ii) MOLECULE TYPE: peptide
233   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
235   Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
236   1           5           10           15
W--> 238   Arg Arg Pro Gln Asp Val Lys Xaa Pro Gly Gly Gly Gln Ile Val Gly
239           20           25           30
241   Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
242           35           40           45

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```

244      Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Asp Arg Arg Gln Pro
245      50                      55                      60
W--> 247      Ile Pro Lys Ala Arg Gln Ser Asp Gly Xaa Xaa Trp Ala Gln Pro Gly
248      65                      70                      75                      80
250      His Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
251      85                      90                      95
253      Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro
254      100                    105
256 (2) INFORMATION FOR SEQ ID NO: 7:
258      (i) SEQUENCE CHARACTERISTICS:
259          (A) LENGTH: 447 base pairs
260          (B) TYPE: nucleic acid
261          (C) STRANDEDNESS: single
262          (D) TOPOLOGY: linear
264      (ii) MOLECULE TYPE: cDNA
266      (iii) HYPOTHETICAL: NO
C--> 268      (iv) ANTI-SENSE: NO
272      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
274 GACGGCGTGA ACTATGCAAC AGGGAATTTG CCTGGTTGCT CTTTCTCTAT CTTCCCTCTTA      60
276 GCTTTTCTGT CCTGCTTGAC GGTTCCTCACT ACCGCTCATG AGGTGCGCAA CGCATCCGGG      120
278 GTATATCATC TCACCAATGA CTGTTCCAAC TCGAGCATCA TCTATGAGAT GAGTGGTATG      180
280 ATCTTGACAG CCCAGGGGTG TGTGCCCTGC GTTCGGGAGA ACAACTCTTC TCGTTGCTGG      240
282 ATGCCRCTCA CCCCCACGCT TGCGGTCAAA GACGCTAATG TCCCTACTGC GGCAATCCGA      300
284 CGCCATGTCG ACTTGCTGGT TGGGACAGCC GCGTTTCGTT CCGCTATGTA CGTGGGGGAC      360
286 CTCTGCGGAT CCGTCTTCCT TGTCGGCCAG CTATTCACCT TTTCACCCCG CTTGTACCAT      420
288 ACAACACAGG AGTGCAACTG CTCAATC      447
290 (2) INFORMATION FOR SEQ ID NO: 8:
292      (i) SEQUENCE CHARACTERISTICS:
293          (A) LENGTH: 149 amino acids
294          (B) TYPE: amino acid
295          (D) TOPOLOGY: linear
297      (ii) MOLECULE TYPE: peptide
301      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
303      Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
304      1          5          10          15
306      Ile Phe Leu Leu Ala Phe Leu Ser Cys Leu Thr Val Pro Thr Thr Ala
307      20          25          30
309      His Glu Val Arg Asn Ala Ser Gly Val Tyr His Leu Thr Asn Asp Cys
310      35          40          45
312      Ser Asn Ser Ser Ile Ile Tyr Glu Met Ser Gly Met Ile Leu His Ala
313      50          55          60
315      Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp
316      65          70          75          80
W--> 318      Met Xaa Leu Thr Pro Thr Leu Ala Val Lys Asp Ala Asn Val Pro Thr
319      85          90          95
321      Ala Ala Ile Arg Arg His Val Asp Leu Leu Val Gly Thr Ala Ala Phe
322      100        105        110
324      Arg Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val
325      115        120        125

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```

327      Gly Gln Leu Phe Thr Phe Ser Pro Arg Leu Tyr His Thr Thr Gln Glu
328          130                      135                      140
330      Cys Asn Cys Ser Ile
331          145
333 (2) INFORMATION FOR SEQ ID NO: 9:
335      (i) SEQUENCE CHARACTERISTICS:
336          (A) LENGTH: 223 base pairs
337          (B) TYPE: nucleic acid
338          (C) STRANDEDNESS: single
339          (D) TOPOLOGY: linear
341      (ii) MOLECULE TYPE: cDNA
343      (iii) HYPOTHETICAL: NO
C--> 345      (iv) ANTI-SENSE: NO
349      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
351 ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAAAGAA ACACCAACCG CCGCCCACAG      60
353 GACGTCAAGT TCCCGGGCGG TGGCCAGATC GTTGGTGGAG TCTACGTGCT ACCGCGCAGG      120
355 GGCCCTAGAT TGGGTGTGCG CGCAGCGCGG AAGACTTCGG AGCGGTCGCA ACCTCGTGGG      180
357 AGGCGCCAAC CTATTCCCAA GGAGCGCCGA CCCGAGGGCA GGT      223
359 (2) INFORMATION FOR SEQ ID NO: 10:
361      (i) SEQUENCE CHARACTERISTICS:
362          (A) LENGTH: 74 amino acids
363          (B) TYPE: amino acid
364          (D) TOPOLOGY: linear
366      (ii) MOLECULE TYPE: peptide
370      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
372 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
373      1          5          10          15
375 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
376          20          25          30
378 Gly Val Tyr Val Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
379          35          40          45
381 Ala Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
382          50          55          60
384 Ile Pro Lys Glu Arg Arg Pro Glu Gly Arg
385          65          70
387 (2) INFORMATION FOR SEQ ID NO: 11:
389      (i) SEQUENCE CHARACTERISTICS:
390          (A) LENGTH: 957 base pairs
391          (B) TYPE: nucleic acid
392          (C) STRANDEDNESS: single
393          (D) TOPOLOGY: linear
395      (ii) MOLECULE TYPE: cDNA
397      (iii) HYPOTHETICAL: NO
C--> 399      (iv) ANTI-SENSE: NO
403      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
405 ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGCA ACACCAACCG CCGCCCACAG      60
407 GACGTTAAAT TCCCGGGTGG GGGGCAGATC GTGGGTGGAG TTTACTTGTT GCCGCGCAGG      120
409 GGCCCCAGGT TGGGTGTGCG CGCGACGAGG AAGACTTCCG AGCGGTCGCA ACCTCGCGGA      180
411 AGGCGACAGC CTATCCCCAA GGCTCGCCGA CCCGAGGGCA GGTCTTGGGC TCAGCCTGGG      240

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Input Set : N:\Crf3\RULE60\09851138A.txt

Output Set: N:\CRF3\12052001\I851138A.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:41 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:45 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:62 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:97 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:127 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:204 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:268 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:345 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:399 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:477 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:480 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:483 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:522 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:586 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:625 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:628 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:631 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:637 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:676 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:751 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:799 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:876 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:929 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1006 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1052 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1073 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1140 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1196 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:1217 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]

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L:1294 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1371 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:1409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:1427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:1430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:1448 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1483 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1525 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1602 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1674 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1677 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1710 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1725 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1803 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1806 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1809 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1818 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1848 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1899 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1902 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1905 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1920 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1989 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:1992 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:1998 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:2004 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:2043 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2077 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:2110 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:2187 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2254 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2321 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2388 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2468 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2535 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2602 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2691 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2758 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2825 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2892 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2959 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:3090 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:3157 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:3224 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:3291 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:3358 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]

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L:3425 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:3492 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:3559 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]